ATTACHMENT A

Amendments to the Specification

Please amend the marked paragraphs in the manner set forth below:

Please amend the paragraph beginning at Page 10, line 11 as follows:

The signal peptides may be identified using any suitable identification method such as that method described in "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites". Henrik Nielsen, Jacob Engelbrecht, Søren Brunak and Gunnar von Heijne, *Protein Engineering* **10**, 1-6 (1997), incorporated herein by reference. In the present process, a preferred system is to ~~us~~use the SignalP prediction server at cbs.dtu.dk/services/SignalP ~~http://www.cbs.dtu.dk/services/SignalP/~~, but other similar methods for identifying the signal peptide may also be used. Location of LPXTG-motif and the determination of positively charged amino acids residues at the C terminus are accomplished using visual examination of the sequence, although databases may also be used to determine the presence of these features..

Please amend the paragraph beginning at Page 10, line 16 as follows:

In the preferred embodiment, the hydrophobic transmembrane segment after the LPXTG-motif may also be located using a conventional program which can predict the presence of such regions. An example of one such system is the TMHMM server available on the Internet at cbs.dtu.dk/services/TMHMM-2.0/ ~~http://www.cbs.dtu.dk/services/ TMHMM-2.0/~~ which can be used for the prediction of transmembrane segments. However, a number of other suitable prediction servers are available either on the Internet or in stored computer programs, including the TMpred available at ch.embnet.org/software/TMPRED_form.html ~~http://www.ch.embnet.org/software/TMPRED_form.html~~, the DAS system available at ww.sbc.su.se/~miklos/DAS/~~http://www.sbc.su.se/~miklos/DAS/~~, and the HMMTOP at www.enzim.hu/hmmtop ~~http://www.enzim.hu/hmmtop/~~.

Please amend the paragraph beginning at Page 11, line 10 as follows:

Similarly, in such a method, LPXTG-containing cell wall proteins may also be located using an annotated genomic nucleotide database such as the one located at the TIGR website (comprehensive microbial resource) at tigr.org/tigr-scripts/CMR2/CMRHomePage.spl http://www.tigr.org/tigr-scripts/CMR2/CMRHomePage.spl. With these databases, the term "LPXTG" or "cell wall" may be used to search for such proteins that are annotated as cell wall anchored proteins in the genome of interest.

Please amend the paragraph beginning at Page 11, line 29 as follows:

In the preferred process of the present invention, steps are carried out by which the Immunoglobulin-like (Ig-like) fold in putative LPXTG-motif containing cell wall anchored proteins can be predicted and identified. In accordance with the invention, the amino acid sequences of putative LPXTG-motif containing cell wall anchored proteins are then analyzed to determine the presence of Ig-like folds which are characteristic of MSCRAMM® proteins. This can be done in a number of ways, such as by processing the putative MSCRAMM® using fold-recognition software, such as available using the web server 3D-PSSM available at sbg.bio.ic.ac.uk/~3dpssm/(~~http://www.sbg.bio.ic.ac.uk/~3dpssm/~~). Additional methods of fold prediction are discussed in Kelley LA, MacCallum RM & Sternberg MJE. Enhanced Genome Annotation using Structural Profiles in the Program 3D-PSSM. J Mol Biol. 2000 Jun 2;299(2):499-520, incorporated herein by reference. Using this method, the output of 3D-PSSM gives a probability E value indicating the likelihood of the submitted sequence adopting a similar 3D structure as the known and published MSCRAMM®s. In accordance with the invention, proteins that have an E value <0.25 to a published Ig-like fold structure, are considered to contain the predicted Ig-like folds, and such proteins are identified as useful MSCRAMM® proteins in accordance with the invention, i.e., proteins that recognize adhesin molecules on the extracellular matrix of host cells.

Please amend the paragraph beginning at Page 45, line 5 as follows:

Signal peptide: we use the SignalP prediction server ~~at http://www.cbs.dtu.dk/services/SignalP/~~. The method has been described in "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites". Henrik Nielsen, Jacob Engelbrecht, Søren Brunak and Gunnar von Heijne, *Protein Engineering* **10**, 1-6 (1997).

Please amend the paragraph beginning at Page 45, line 11 as follows:

A hydrophobic transmembrane segment after the LPXTG-motif: we use the TMHMM server ~~at http://www.cbs.dtu.dk/services/TMHMM-2.0/~~ for the prediction of transmembrane segments. Several other prediction web servers can also be used, among which are TMpred ~~at http://www.ch.embnet.org/software/TMPRED_form.html~~, DAS ~~at http://www.sbc.su.se/~miklos/DAS/~~, and HMMTOP ~~at http://www.enzim.hu/hmmtop/~~.

Please amend the paragraph beginning at Page 46, line 11 as follows:

The amino acid sequences of putative LPXTG-motif containing cell wall anchored proteins are submitted to a Fold recognition web server 3D-PSSM ~~(http://www.sbg.bio.ic.ac.uk/~3dpssm/)~~. The method of prediction is described in Kelley LA, MacCallum RM & Sternberg MJE. Enhanced Genome Annotation using Structural Profiles in the Program 3D-PSSM. J Mol Biol. 2000 Jun 2;299(2):499-520

Please amend the paragraph beginning at Page 54, line 12 as follows:

EF1093 amino acid residues 33-~~590~~592 (SEQ ID NO:13)

0 MKQLKKVWYT VSTLLLILPL FTSVLGTTTA FA**EENGESAQ LVIHKKKMTD**
50 LPDPLIQNSG KEMSEFDKYQ GLADVTFSIY NVTNEFYEQR AAGASVDAAK
100 QAVQSLTPGK PVAQGTTDAN GNVTVQLPKK QNGKDAVYTI KEEPKEGVVA
150 ATNMVVAFPV YEMIKQTDGS YKYGTEELAV VHIYPKNVVA NDGSLHVKKV
200 GTAENEGLNG AEFVISKSEG SPGTVKYIQG VKDGLYTWTT DKEQAKRFIT
250 GKSYEIGEND FTEAENGTGE LTVKNLEVGS YILEEVKAPN NAELIENQTK
300 TPFTIEANNQ TPVEKTVKND TSKVDKTTPS LDGKDVAIGE KIKYQISVNI
350 PLGIADKEGD ANKYVKFNLV DKHDAALTFD NVTSGEYAYA LYDGDTVIAP
400 ENYQVTEQAN GFTVAVNPAY IPTLTPGGTL KFVYFMHLNE KADPTKGFKN
450 EANVDNGHTD DQTPPTVEVV TGGKRFIKVD GDVTATQALA GASFVVRDQN
500 SDTANYLKID ETTKAATWVK TKAEATTFTT TADGLVDITG LKYGTYYLEE
550 TVAPDDYVLL TNRIEFVVNE QSYGTTENLV SPEKVPNKHK GTLPSTGGKG
600 IYVYLGSGAV LLLIAGVYFA RRRKENA

Please amend the paragraph beginning at Page 61, line 16 as follows:

The "A" domain amino acid sequence from each *E. faecalis* MSCRAMM® protein was used as a query in a blastp ~~(http://www.ncbi.nlm.nih. gov/ BLAST/)~~ search. Results shown were scored by NCBI computers. Identity is calculated as exact matches between the subject and query sequences while similarity also includes conservative changes in sequence at the same position.